

1600

Skuse
 RAW SEQUENCE LISTING DATE: 09/07/2001
 PATENT APPLICATION: US/09/597,796A TIME: 13:55:04

Input Set : A:\-90-7pc.app
 Output Set: N:\CRF3\09072001\I597796A.raw

3 <110> APPLICANT: Skeiky, Yasir
 4 Reed, Steven
 5 Alderson, Mark
 6 Corixa Corporation
 8 <120> TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
 10 <130> FILE REFERENCE: 014058-009070PC
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/597,796A
 C--> 13 <141> CURRENT FILING DATE: 2000-06-20
 15 <150> PRIOR APPLICATION NUMBER: US 09/597,796
 16 <151> PRIOR FILING DATE: 2000-06-20
 18 <150> PRIOR APPLICATION NUMBER: US 60/265,737
 19 <151> PRIOR FILING DATE: 2001-02-01
 21 <160> NUMBER OF SEQ ID NOS: 49
 23 <170> SOFTWARE: PatentIn Ver. 2.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1872
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Mycobacterium tuberculosis
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: MTB32A (Ra35FL)
 33 <220> FEATURE:
 34 <221> NAME/KEY: modified_base
 35 <222> LOCATION: (1)..(1872)
 36 <223> OTHER INFORMATION: n = g, a, c or t
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 41 gtcatggtt ctgagcgtgc tggctgccgt cgggctggc ctggccacgg cgccggccca 180
 42 gggggccccc cggcccttgc cgaggaccg gttccgcac ttccccgcgc tgccctcga 240
 43 cccgtccgcg atggtcgccc aagtggcgcc acagggtggc aacatcaaca ccaaactggg 300
 44 ctacaacaac gccgtggcgcc cggggaccgg catcgatc gatccaaacg gtgtcgtgt 360
 45 gaccaacaac cacgtatcg cgggcgcac cggatcgatc ggttccggc tgggtccgg 420
 46 ccaaaccatac ggcgtcgatg tggctggta tgaccgcacc caggatgtcg cgggtctgca 480
 47 gctgcgcggt gccgggtggcc tggctcgccg ggcgtcggt ggcggcgctcg cgggtgggtga 540
 48 gccgcgtc gcatggggca acaggcggtgg cggggcgga acggcccccgtg cgggtccctgg 600
 49 cagggtggtc ggcgtcgcc aaaccgtgca ggcgtcgat tggctgaccg gtgcgaaga 660
 50 gacattgaac gggttgatcc agttcgatgc cgcaatccag cccgtgatt cggggccggcc 720
 51 cgtcgtaac ggcctaggac aggtggtcgg tatgaacacg gccgcgtccg ataacttcca 780
 52 gctgtccca ggtgggcagg gattcgccat tccgatcggtt caggcgatgg cgatcgccgg 840
 53 ccaaatccga tcgggtgggg ggtcacccac cgatcgatc gggcttaccc ctttcctcgg 900
 54 cttgggtgtt gtcgacaaca acggcaacgg cgacgagtc caacgcgtgg tcggaaagcgc 960
 55 tccggcgca agtctcgca tctccaccgg cgacgtgatc accgcggctcg acggcgctcc 1020
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 57 ctcggtaac tggcaaaacca agtcggcgacg caccgtaca gggaaacgtga cattggccga 1140
 58 gggacccccc gctgtatcc tcgcggatcc caccgcggc cggccaaatt ggattggcgc 1200
 59 cagccgtat tggcgatcc gccccccgat tccgtctccc gtgcgcgtgg cattgtggaa 1260
 60 gcaatgaacg aggcaaca cagcgtttag caccctcccg tgcaggccag ttacgtcga 1320

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61 ggcggtgtgg tcgagcatcc ggatgccaag gacttcggca gcgcgcgcgc cctgcccgc 1380
 62 gatccgacct ggttaagca cgccgtttc tacgaggtgc tggccggc gttttcgac 1440
 W--> 63 gccagcgcgg acggttccgn cgatctgcgt ggactcatcg atcgccctcga ctacactgcag 1500
 64 tggcttggca tcgactgcat ctgttgcgc cgttctacg actcaccgct gcgcgacggc 1560
 65 ggttacgaca ttgcgactt ctacaagggtg ctgcccgaat tcggcaccgt cgacgatttc 1620
 66 gtcgcctgg tcgacaccgc tcacccggca ggtatccgca tcacccggca cctgtgtatg 1680
 67 aatcacacact cggagtcgca cccctggttt caggagtcggcc gccgcgaccc agacggaccg 1740
 W--> 68 tacgggtact attacgtgtg gagcgacacc agcgagcgct acaccgacgc ccggatcatc 1800
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 75 <212> TYPE: PRT
 76 <213> ORGANISM: Mycobacterium tuberculosis
 78 <220> FEATURE:
 79 <223> OTHER INFORMATION: MTB32A (Ra35FL)
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 85 Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
 86 20 25 30
 88 Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
 89 35 40 45
 91 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
 92 50 55 60
 94 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 95 65 70 75 80
 97 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 98 85 90 95
 100 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 101 100 105 110
 103 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 104 115 120 125
 106 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 107 130 135 140
 109 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 110 145 150 155 160
 112 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 113 165 170 175
 115 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 116 180 185 190
 118 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 119 195 200 205
 121 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 122 210 215 220
 124 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 125 225 230 235 240
 127 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 128 245 250 255

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Input Set : A:\-90-7pc.app
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130 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
131 260 265 270
133 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
134 275 280 285
136 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
137 290 295 300
139 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
140 305 310 315 320
142 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
143 325 330 335
145 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
146 340 345 350
148 Pro Pro Ala
149 355
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153 <211> LENGTH: 1002
154 <212> TYPE: DNA
155 <213> ORGANISM: Mycobacterium tuberculosis
157 <220> FEATURE:
158 <223> OTHER INFORMATION: MTB32A (Ra35 mature)
160 <400> SEQUENCE: 3
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162 ttcccccgcgc tgcccttcga cccgtccgcg atggtcgcgc aagtggggcc acagggtggtc 120
163 aacatcaaca ccaaactggg ctacaacaac gccgtggcg ccgggaccgg catcgatcatc 180
164 gatcccaacg gtgtcggtct gaccaacaac cacgtatcg cgccgcgcac cgacatcaat 240
165 gcgttcagcg tcggctccgg ccaaaccctac ggcgtcgatg tggtcggta tgaccgcacc 300
166 caggatgtcg cgggtgtcgca gctgcgcgtg gccgtggcc tgccgtcgcc ggcgatcggt 360
167 ggcggcgtcg cgggtggta gcccgtcgcc gcgatggca acagcggtgg gcagggcgga 420
168 acgccccgtg cgggtccctgg cagggtggtc ggcgtcgcc aaaccgtgca ggcgtcgat 480
169 tcgctgaccc gtgcggaaaga gacattgaac ggggtatcc agttcgatgc cgccatccag 540
170 cccgggtgagg cggggggggcc cgtcgtaac ggcctaggac aggtggtcgg tatgaacacg 600
171 gccgcgtccg ataacttcca gctgtcccag ggtgggcagg gattcgccat tccgatcggt 660
172 caggcgatgg cgatcgcggg ccagatccga tcgggtgggg ggtcaccac cgttcatatc 720
173 gggcctaccc ctttcctcggtt gtcgacaaca acggcaacgg cgacacgatc 780
174 caacgcgtgg tcgggagcgc tccggcggca agtctcggtc tctccacccg cgacgtgtatc 840
175 accgcggctcg acggcgctcc gatcaactcg gccaccgcga tggcggacgc gcttaacggg 900
176 catcatcccg gtgacgtcat ctcggtgacc tggcaaaccg agtcggccgg cacgcgtaca 960
177 gggAACGTGA CATTGGCCGA GGGACCCCCG GCCTGAGAAT TC 1002
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181 <211> LENGTH: 330
182 <212> TYPE: PRT
183 <213> ORGANISM: Mycobacterium tuberculosis
185 <220> FEATURE:
186 <223> OTHER INFORMATION: MTB32A (Ra35 mature)
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192 Phe Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala
193 20 25 30

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Input Set : A:\-90-7pc.app
Output Set: N:\CRF3\09072001\I597796A.raw

195 Gln Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn
196 35 40 45
198 Asn Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val
199 50 55 60
201 Val Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala
202 65 70 75 80
204 Phe Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr
205 85 90 95
207 Asp Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly
208 100 105 110
210 Leu Pro Ser Ala Ala Ile Gly Gly Val Ala Val Gly Glu Pro Val
211 115 120 125
213 Val Ala Met Gly Asn Ser Gly Gln Gly Gly Thr Pro Arg Ala Val
214 130 135 140
216 Pro Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser
217 145 150 155 160
219 Leu Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala
220 165 170 175
222 Ala Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly
223 180 185 190
225 Gln Val Val Gly Met Asn Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser
226 195 200 205
228 Gln Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile
229 210 215 220
231 Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile Gly
232 225 230 235 240
234 Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly
235 245 250 255
237 Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly
238 260 265 270
240 Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn
241 275 280 285
243 Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp
244 290 295 300
246 Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly
247 305 310 315 320
249 Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
250 325 330
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254 <211> LENGTH: 1002
255 <212> TYPE: DNA
256 <213> ORGANISM: Artificial Sequence
258 <220> FEATURE:
259 <223> OTHER INFORMATION: Description of Artificial Sequence: Ra35FLMutSA
261 <400> SEQUENCE: 5
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263 ttccccgcgc tgccccctcga cccgtccgcg atggtcgccc aagtggggcc acaggtggtc 120
264 aacatcaaca ccaaactggg ctacaacaac gccgtggcgc ccgggaccgg catcgatc 180
265 gatcccaacg gtgtcgtgct gaccaacaac cacgtatcg cggcgccac cgacatcaat 240

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Input Set : A:\-90-7pc.app
Output Set: N:\CRF3\09072001\I597796A.raw

266 gcgttcagcg tcggctccgg ccaaacc tac ggcgtcgatg tggtcggta tgaccgcacc 300
 267 caggatgtcg cggctcgca gctgcgcgtt gcccgtggc tgccgtcggc ggcgatcggt 360
 268 ggcggcgtcg cggttggta gcccgtcgca gcgatggca acagcggtgg gcaaggcgga 420
 269 acgccccgtg cggtgctgg caggggtggc ggcgtcggcc aaaccgtgca ggcgtcggat 480
 270 tcgctgaccg gtgcggaaaga gacattgaac gggttgatcc agttcgatgc cgcgatccag 540
 271 cccggtgatg cggggggcc cgtcgtaac ggcctaggac aggtggtcgg tatgaacacg 600
 272 gcccgtccg ataacttcca gctgtcccag ggtgggcagg gattcgccat tccgatcggg 660
 273 caggcgatgg cgatcgccgg ccagatccga tcgggtggg ggtcaccac cgttcatatc 720
 274 gggcctaccc cttctctcggtt gtcgacaaca acggcaacgg cgcacgagtc 780
 275 caacgcgtgg tcgggagcgc tccggcggca agtctcggca tctccaccgg cgacgtgatc 840
 276 accgcggtcg acggcgctcc gatcaactcg gccaccgcga tggcggacgc gcttaacggg 900
 277 catcatcccg gtgacgtcat ctcggtggacc tggcaaaccg agtcggcgg cacgcgtaca 960
 278 gggAACGTGA cattggccga gggacccccc gcctgagaat tc 1002
 281 <210> SEQ ID NO: 6
 282 <211> LENGTH: 330
 283 <212> TYPE: PRT
 284 <213> ORGANISM: Artificial Sequence
 285 <220> FEATURE:
 287 <223> OTHER INFORMATION: Description of Artificial Sequence: Ra35FLMutSA
 289 <400> SEQUENCE: 6
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 291 1 5 10 15
 293 Phe Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala
 294 20 25 30
 296 Gln Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn
 297 35 40 45
 299 Asn Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val
 300 50 55 60
 302 Val Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala
 303 65 70 75 80
 305 Phe Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr
 306 85 90 95
 308 Asp Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly
 309 100 105 110
 311 Leu Pro Ser Ala Ala Ile Gly Gly Val Ala Val Gly Glu Pro Val
 312 115 120 125
 314 Val Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val
 315 130 135 140
 317 Pro Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser
 318 145 150 155 160
 320 Leu Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala
 321 165 170 175
 323 Ala Ile Gln Pro Gly Asp Ala Gly Gly Pro Val Val Asn Gly Leu Gly
 324 180 185 190
 326 Gln Val Val Gly Met Asn Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser
 327 195 200 205
 329 Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile
 330 210 215 220
 332 Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile Gly

FYI
Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa.

VERIFICATION SUMMARY
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Input Set : A:\-90-7pc.app
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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:63 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:69 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:506 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:570 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:755 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:939 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:941 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:950 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1464 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1704 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1714 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1720 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1721 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1743 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:2164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:2442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:2444 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:2447 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:2448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
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L:2486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:2516 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
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L:2666 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:2930 M:258 W: Mandatory Feature missing, <220> FEATURE: